Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (Currently amended) A method for analyzing activation pathways controlled by neurotransmitters comprising,

(i) obtaining a nucleic acid from a biological sample;

(ii) contacting the nucleic acid with a micro-array comprising capture probes derived from the 5 major subfamilies of amine neurotransmitter receptors, under conditions allowing hybridization of complementary strands; and

(iii) analyzing a two dimensional pattern of data present as intensities of spots on the surface of a support of the micro-array, one spot being sufficient for obtaining the information on one neurotransmitter subtype,

wherein said 5 major subfamilies of amine neurotransmitter receptors are dopamine, histamine, serotonin, adrenergic and cholinergic receptors.

2. (Original) The method according to claim 1, wherein the micro-array comprises capture probes specific for at least 2 subtypes of dopamine receptors, 2 subtypes of histamine receptors, 4 subtypes of serotonin receptors, 2 subtypes of adrenergic receptors and 4 subtypes of cholinergic receptors.

3. (Currently amended) The method according to claim 1, wherein the micro-array comprises capture probes for at least 20 different subtypes ~~or sub-subtypes~~ among the 5 subtypes for dopamine, 4 subtypes for histamine, 14 subtypes for serotonin, 5 subtypes for adrenergic and 16 subtypes for cholinergic,

wherein the 16 subtypes for cholinergic are CHRM1, CHRM2, CHRM3, CHRM4, CHRM5, CHRNA2, CHRNA3, CHRNA4, CHRNA5, CHRNA7, CHRNB1, CHRNB2, CHRNB3, CHRNB4, CHRND and CHRNE.

4. (Currently amended) The method according to claim 3, wherein the micro-array further comprises capture probes for the detection of 1 subtype of octopamine and the 14 subtypes of trace amines,

wherein the 14 subtypes of trace amines are TA1, TA2, TA3, TA4, TA6, TA7, TA8, TA9, TA10, TA11, TA12, TA13, TA14 and TA15.

5. (Original) The method according to claim 1, wherein the capture probes are derived from the list in table 1.

6. (Original) The method according to claim 1, wherein the capture probes are derived from the sense or from the antisense strand of the gene encoding the receptor.

7. (Original) The method according to claim 1, wherein the target nucleic acid derived from a biological sample is RNA or cDNA.

8. (Original) The method according to claim 1, wherein the nucleic acid is labeled during synthesis of cDNA.

9. (Original) The method according to claim 8, wherein the label comprises fluorescent dyes, radiolabels, enzymes or colorimetric labels.

10-30. (Cancelled)